

1/31



OIPE

## RAW SEQUENCE LISTING

DATE: 01/27/2002

PATENT APPLICATION: US/10/039,073

TIME: 15:30:11

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\01272002\J039073.raw

ENTERED

4 <110> APPLICANT: Kapeller-Libermann, Rosana  
 5 Williamson, Mark  
 7 <120> TITLE OF INVENTION: 17867, A Novel Human Aminopeptidase  
 10 <130> FILE REFERENCE: 35800/240749(5800-36  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/039,073  
 C--> 12 <141> CURRENT FILING DATE: 2001-12-31  
 12 <150> PRIOR APPLICATION NUMBER: 09/345,650  
 13 <151> PRIOR FILING DATE: 1999-06-30  
 15 <160> NUMBER OF SEQ ID NOS: 3  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 960  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Homo sapiens  
 24 <400> SEQUENCE: 1  
 25 Met Phe His Ser Ser Ala Met Val Asn Ser His Arg Lys Pro Met Phe  
 26 1 5 10 15  
 27 Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile Leu Pro Gln Ile  
 28 20 25 30  
 29 Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu  
 30 35 40 45  
 31 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp  
 32 50 55 60  
 33 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu  
 34 65 70 75 80  
 35 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys  
 36 85 90 95  
 37 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser  
 38 100 105 110  
 39 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser  
 40 115 120 125  
 41 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala  
 42 130 135 140  
 43 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu  
 44 145 150 155 160  
 45 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe  
 46 165 170 175  
 47 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg  
 48 180 185 190  
 49 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe  
 50 195 200 205  
 51 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile  
 52 210 215 220

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```

53 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Lys
54 225                230                235                240
55 Thr Ile Glu Leu Glu Gly Gly Leu Leu Glu Asp His Phe Glu Thr Thr
56                245                250                255
57 Val Lys Met Ser Thr Tyr Leu Val Ala Tyr Ile Val Cys Asp Phe His
58                260                265                270
59 Ser Leu Ser Gly Phe Thr Ser Ser Gly Val Lys Val Ser Ile Tyr Ala
60                275                280                285
61 Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln Ala Ser Leu
62                290                295                300
63 Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr Tyr Pro Leu
64 305                310                315                320
65 Ser Lys Leu Asp Leu Ile Ala Ile Pro Asp Phe Ala Pro Gly Ala Met
66                325                330                335
67 Glu Asn Trp Gly Leu Ile Thr Tyr Arg Glu Thr Ser Leu Leu Phe Asp
68                340                345                350
69 Pro Lys Thr Ser Ser Ala Ser Asp Lys Leu Trp Val Thr Arg Val Ile
70                355                360                365
71 Ala His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr Met Glu
72                370                375                380
73 Trp Trp Asn Asp Ile Trp Leu Lys Glu Gly Phe Ala Lys Tyr Met Glu
74 385                390                395                400
75 Leu Ile Ala Val Asn Ala Thr Tyr Pro Glu Leu Gln Phe Asp Asp Tyr
76                405                410                415
77 Phe Leu Asn Val Cys Phe Glu Val Ile Thr Lys Asp Ser Leu Asn Ser
78                420                425                430
79 Ser Arg Pro Ile Ser Lys Pro Ala Glu Thr Pro Thr Gln Ile Gln Glu
80                435                440                445
81 Met Phe Asp Glu Val Ser Tyr Asn Lys Gly Ala Cys Ile Leu Asn Met
82                450                455                460
83 Leu Lys Asp Phe Leu Gly Glu Glu Lys Phe Gln Lys Gly Ile Ile Gln
84 465                470                475                480
85 Tyr Leu Lys Lys Phe Ser Tyr Arg Asn Ala Lys Asn Asp Asp Leu Trp
86                485                490                495
87 Ser Ser Leu Ser Asn Ser Cys Leu Glu Ser Asp Phe Thr Ser Gly Gly
88                500                505                510
89 Val Cys His Ser Asp Pro Lys Met Thr Ser Asn Met Leu Ala Phe Leu
90                515                520                525
91 Gly Glu Asn Ala Glu Val Lys Glu Met Met Thr Thr Trp Thr Leu Gln
92                530                535                540
93 Lys Gly Ile Pro Leu Leu Val Val Lys Gln Asp Gly Cys Ser Leu Arg
94 545                550                555                560
95 Leu Gln Gln Glu Arg Phe Leu Gln Gly Val Phe Gln Glu Asp Pro Glu
96                565                570                575
97 Trp Arg Ala Leu Gln Glu Arg Tyr Leu Trp His Ile Pro Leu Thr Tyr
98                580                585                590
99 Ser Thr Ser Ser Ser Asn Val Ile His Arg His Ile Leu Lys Ser Lys
100                595                600                605
101 Thr Asp Thr Leu Asp Leu Pro Glu Lys Thr Ser Trp Val Lys Phe Asn

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102      610      615      620
103 Val Asp Ser Asn Gly Tyr Tyr Ile Val His Tyr Glu Gly His Gly Trp
104 625      630      635      640
105 Asp Gln Leu Ile Thr Gln Leu Asn Gln Asn His Thr Leu Leu Arg Pro
106      645      650      655
107 Lys Asp Arg Val Gly Leu Ile His Asp Val Phe Gln Leu Val Gly Ala
108      660      665      670
109 Gly Arg Leu Thr Leu Asp Lys Ala Leu Asp Met Thr Tyr Tyr Leu Gln
110      675      680      685
111 His Glu Thr Ser Ser Pro Ala Leu Leu Glu Gly Leu Ser Tyr Leu Glu
112      690      695      700
113 Ser Phe Tyr His Met Met Asp Arg Arg Asn Ile Ser Asp Ile Ser Glu
114 705      710      715      720
115 Asn Leu Lys Arg Tyr Leu Leu Gln Tyr Phe Lys Pro Val Ile Asp Arg
116      725      730      735
117 Gln Ser Trp Ser Asp Lys Gly Ser Val Trp Asp Arg Met Leu Arg Ser
118      740      745      750
119 Ala Leu Leu Lys Leu Ala Cys Asp Leu Asn His Ala Pro Cys Ile Gln
120      755      760      765
121 Lys Ala Ala Glu Leu Phe Ser Gln Trp Met Glu Ser Ser Gly Lys Leu
122      770      775      780
123 Asn Ile Pro Thr Asp Val Leu Lys Ile Val Tyr Ser Val Gly Ala Gln
124 785      790      795      800
125 Thr Thr Ala Gly Trp Asn Tyr Leu Leu Glu Gln Tyr Glu Leu Ser Met
126      805      810      815
127 Ser Ser Ala Glu Gln Asn Lys Ile Leu Tyr Ala Leu Ser Thr Ser Lys
128      820      825      830
129 His Gln Glu Lys Leu Leu Lys Leu Ile Glu Leu Gly Met Glu Gly Lys
130      835      840      845
131 Val Ile Lys Thr Gln Asn Leu Ala Ala Leu Leu His Ala Ile Ala Arg
132      850      855      860
133 Arg Pro Lys Gly Gln Gln Leu Ala Trp Asp Phe Val Arg Glu Asn Trp
134 865      870      875      880
135 Thr His Leu Leu Lys Lys Phe Asp Leu Gly Ser Tyr Asp Ile Arg Met
136      885      890      895
137 Ile Ile Ser Gly Thr Thr Ala His Phe Ser Ser Lys Asp Lys Leu Gln
138      900      905      910
139 Glu Val Lys Leu Phe Phe Glu Ser Leu Glu Ala Gln Gly Ser His Leu
140      915      920      925
141 Asp Ile Phe Gln Thr Val Leu Glu Thr Ile Thr Lys Asn Ile Lys Trp
142      930      935      940
143 Leu Glu Lys Asn Leu Pro Thr Leu Arg Thr Trp Leu Met Val Asn Thr
144 945      950      955      960
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 3366
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
152 <220> FEATURE:
153 <221> NAME/KEY: CDS

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154 &lt;222&gt; LOCATION: (146)...(3028)

156 &lt;400&gt; SEQUENCE: 2

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157 ccccgcgctcc ggcattgattt aagattaaat tcatgtattg aaaatattgt tcagacccca 60
158 tgtgacataa ctggagccag tgcagtgcc tgaagaacta cgagattagc ctggatatta 120
159 acttgtotc tagagaatag atttc atg ttc cat tct tct gca atg gtt aat 172
160 Met Phe His Ser Ser Ala Met Val Asn
161 1 5
163 tca cac aga aaa cca atg ttt aac att cac aga gga ttt tac tgc tta 220
164 Ser His Arg Lys Pro Met Phe Asn Ile His Arg Gly Phe Tyr Cys Leu
165 10 15 20 25
167 aca gcc atc ttg ccc caa ata tgc att tgt tct cag ttc tca gtg cca 268
168 Thr Ala Ile Leu Pro Gln Ile Cys Ile Cys Ser Gln Phe Ser Val Pro
169 30 35 40
171 tct agt tat cac ttc act gag gat cct ggg gct ttc cca gta gcc act 316
172 Ser Ser Tyr His Phe Thr Glu Asp Pro Gly Ala Phe Pro Val Ala Thr
173 45 50 55
175 aat ggg gaa cga ttt cct tgg cag gag cta agg ctc ccc agt gtg gtc 364
176 Asn Gly Glu Arg Phe Pro Trp Gln Glu Leu Arg Leu Pro Ser Val Val
177 60 65 70
179 att cct ctc cat tat gac ctc ttt gtc cac ccc aat ctc acc tct ctg 412
180 Ile Pro Leu His Tyr Asp Leu Phe Val His Pro Asn Leu Thr Ser Leu
181 75 80 85
183 gac ttt gtt gca tct gag aag atc gaa gtc ttg gtc agc aat gct acc 460
184 Asp Phe Val Ala Ser Glu Lys Ile Glu Val Leu Val Ser Asn Ala Thr
185 90 95 100 105
187 cag ttt atc atc ttg cac agc aaa gat ctt gaa atc acg aat gcc acc 508
188 Gln Phe Ile Ile Leu His Ser Lys Asp Leu Glu Ile Thr Asn Ala Thr
189 110 115 120
191 ctt cag tca gag gaa gat tca aga tac atg aaa cca gga aaa gaa ctg 556
192 Leu Gln Ser Glu Glu Asp Ser Arg Tyr Met Lys Pro Gly Lys Glu Leu
193 125 130 135
195 aaa gtt ttg agt tac cct gct cat gaa caa att gca ctg ctg gtt cca 604
196 Lys Val Leu Ser Tyr Pro Ala His Glu Gln Ile Ala Leu Leu Val Pro
197 140 145 150
199 gag aaa ctt acg cct cac ctg aaa tac tat gtg gct atg gac ttc caa 652
200 Glu Lys Leu Thr Pro His Leu Lys Tyr Tyr Val Ala Met Asp Phe Gln
201 155 160 165
203 gcc aag tta ggt gat ggc ttt gaa ggg ttt tat aaa agc aca tac aga 700
204 Ala Lys Leu Gly Asp Gly Phe Glu Gly Phe Tyr Lys Ser Thr Tyr Arg
205 170 175 180 185
207 act ctt ggt ggt gaa aca aga att ctt gca gta aca gat ttt gag cca 748
208 Thr Leu Gly Gly Glu Thr Arg Ile Leu Ala Val Thr Asp Phe Glu Pro
209 190 195 200
211 acc cag gca cgc atg gct ttc cct tgc ttt gat gaa ccg ttg ttc aaa 796
212 Thr Gln Ala Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Leu Phe Lys
213 205 210 215
215 gcc aac ttt tca atc aag ata cga aga gag agc agg cat att gca cta 844
216 Ala Asn Phe Ser Ile Lys Ile Arg Arg Glu Ser Arg His Ile Ala Leu
217 220 225 230

```

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```

219 tcc aac atg cca aag gtt aag aca att gaa ctt gaa gga ggt ctt ttg      892
220 Ser Asn Met Pro Lys Val Lys Thr Ile Glu Leu Glu Gly Gly Leu Leu
221      235                      240                      245
223 gaa gat cac ttt gaa act act gta aaa atg agt aca tac ctt gta gcc      940
224 Glu Asp His Phe Glu Thr Thr Val Lys Met Ser Thr Tyr Leu Val Ala
225 250                      255                      260                      265
227 tac ata gtt tgt gat ttc cac tct ctg agt ggc ttc act tca tca ggg      988
228 Tyr Ile Val Cys Asp Phe His Ser Leu Ser Gly Phe Thr Ser Ser Gly
229      270                      275                      280
231 gtc aag gtg tcc atc tat gca tcc cca gac aaa cgg aat caa aca cat      1036
232 Val Lys Val Ser Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His
233      285                      290                      295
235 tat gct ttg cag gca tca ctg aag cta ctt gat ttt tat gaa aag tac      1084
236 Tyr Ala Leu Gln Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr
237      300                      305                      310
239 ttt gat atc tac tat cca ctc tcc aaa ctg gat tta att gct att cct      1132
240 Phe Asp Ile Tyr Tyr Pro Leu Ser Lys Leu Asp Leu Ile Ala Ile Pro
241      315                      320                      325
243 gac ttt gca cct gga gcc atg gaa aat tgg ggc ctc att aca tat agg      1180
244 Asp Phe Ala Pro Gly Ala Met Glu Asn Trp Gly Leu Ile Thr Tyr Arg
245 330                      335                      340                      345
247 gag acg tca ctg ctt ttt gac ccc aag acc tct tct gct tcc gat aaa      1228
248 Glu Thr Ser Leu Leu Phe Asp Pro Lys Thr Ser Ser Ala Ser Asp Lys
249      350                      355                      360
251 ctg tgg gtc acc aga gtc ata gcc cat gaa ctg gcg cac cag tgg ttt      1276
252 Leu Trp Val Thr Arg Val Ile Ala His Glu Leu Ala His Gln Trp Phe
253      365                      370                      375
255 ggc aac ctg gtc aca atg gaa tgg tgg aat gat att tgg ctt aag gag      1324
256 Gly Asn Leu Val Thr Met Glu Trp Trp Asn Asp Ile Trp Leu Lys Glu
257      380                      385                      390
259 ggt ttt gca aaa tac atg gaa ctt atc gct gtt aat gct aca tat cca      1372
260 Gly Phe Ala Lys Tyr Met Glu Leu Ile Ala Val Asn Ala Thr Tyr Pro
261      395                      400                      405
263 gag ctg caa ttt gat gac tat ttt ttg aat gtg tgt ttt gaa gta att      1420
264 Glu Leu Gln Phe Asp Asp Tyr Phe Leu Asn Val Cys Phe Glu Val Ile
265 410                      415                      420                      425
267 aca aaa gat tca ttg aat tca tcc cgc cct atc tcc aaa cca gcg gaa      1468
268 Thr Lys Asp Ser Leu Asn Ser Ser Arg Pro Ile Ser Lys Pro Ala Glu
269      430                      435                      440
271 acc ccg act caa ata cag gaa atg ttt gat gaa gtt tcc tat aac aag      1516
272 Thr Pro Thr Gln Ile Gln Glu Met Phe Asp Glu Val Ser Tyr Asn Lys
273      445                      450                      455
275 gga gct tgt att ttg aat atg ctc aag gat ttt ctg ggt gag gag aaa      1564
276 Gly Ala Cys Ile Leu Asn Met Leu Lys Asp Phe Leu Gly Glu Glu Lys
277      460                      465                      470
279 ttc cag aaa gga ata att cag tac tta aag aag ttc agc tat aga aat      1612
280 Phe Gln Lys Gly Ile Ile Gln Tyr Leu Lys Lys Phe Ser Tyr Arg Asn
281      475                      480                      485
283 gct aag aat gat gac ttg tgg agc agt ctg tca aat agt tgt tta gaa      1660

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/039,073

DATE: 01/27/2002

TIME: 15:30:12

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\01272002\J039073.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date